



IFWO

RAW SEQUENCE LISTING

DATE: 08/27/2004

PATENT APPLICATION: US/10/700,313

TIME: 14:23:00

Input Set : N:\Crf3\RULE60\10700313.raw

Output Set: N:\CRF4\08272004\J700313.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Combadiere et al.,
- 7 (ii) TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
- 9 (iii) NUMBER OF SEQUENCES: 9
- 11 (iv) CORRESPONDENCE ADDRESS:
 - 12 (A) ADDRESSEE: Fish & Richardson P.C.
 - 13 (B) STREET: 4225 Executive Square, Suite 1400
 - 14 (C) CITY: La Jolla
 - 15 (D) STATE: CA
 - 16 (E) COUNTRY: USA
 - 17 (F) ZIP: 92037

19 (v) COMPUTER READABLE FORM:

- 20 (A) MEDIUM TYPE: Floppy disk
- 21 (B) COMPUTER: IBM PC compatible
- 22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

25 (vi) CURRENT APPLICATION DATA:

- C--> 26 (A) APPLICATION NUMBER: US/10/700,313
- C--> 27 (B) FILING DATE: 31-Oct-2003
- W--> 37 (C) CLASSIFICATION: 536

C--> 34 (vii) PRIOR APPLICATION DATA:

- 31 (A) APPLICATION NUMBER: US/08/864,458
- 32 (B) FILING DATE: 28-MAY-1997
- 35 (A) APPLICATION NUMBER: Provisional 60/018,508
- 36 (B) FILING DATE: May 28, 1996

C--> 39 (viii) ATTORNEY/AGENT INFORMATION:

- 40 (A) NAME: Haile, Lisa A.
- 41 (B) REGISTRATION NUMBER: 38,347
- 42 (C) REFERENCE/DOCKET NUMBER: 08830/030001

C--> 44 (ix) TELECOMMUNICATION INFORMATION:

- 45 (A) TELEPHONE: 619/678-5070
- 46 (B) TELEFAX: 619/678-5099

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:

- 52 (A) LENGTH: 1225 base pairs
- 53 (B) TYPE: nucleic acid
- 54 (C) STRANDEDNESS: single
- 55 (D) TOPOLOGY: linear

57 (ii) MOLECULE TYPE: cDNA

61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

63 AAGAAACTCT CCCCAGGTGG AACAAG 26

65 ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA 74

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66 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
67 1 5 10 15
69 TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC 122
70 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
71 20 25 30
72 CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC 170
73 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
74 35 40 45
76 ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG 218
77 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
78 50 55 60
80 ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT 266
81 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
82 65 70 75 80
84 CTT ACT GTC CCC TTC TGG GCT CAC TAC TTG GCC GCC CAG TGG GAC TTT 314
85 Leu Thr Val Pro Phe Trp Ala His Tyr Leu Ala Ala Gln Trp Asp Phe
86 85 90 95
88 GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC 362
89 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
90 100 105 110
92 TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG 410
93 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
94 115 120 125
96 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT 458
97 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
98 130 135 140
100 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT 506
101 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
102 145 150 155 160
104 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC 554
105 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
106 165 170 175
108 ACC TGC AGC TCT CAT TTT CCA TAC AGT CAG TAT CAA TTC TGG AAG AAT 602
109 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
110 180 185 190
112 TTC CAG ACA TTA AAG ATA GTC ATC TTG GGG CTG GTC CTG CCG CTG CTT 650
113 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
114 195 200 205
116 GTC ATG GTC ATC TGC TAC TCG GGA ATC CTA AAA ACT CTG CTT CGG TGT 698
117 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
118 210 215 220
120 CGA AAT GAG AAG AAG AGG CAC AGG GCT GTG AGG CTT ATC TTC ACC ATC 746
121 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
122 225 230 235 240
124 ATG ATT GTT TAT TTT CTC TTC TGG GCT CCC TAC AAC ATT GTC CTT CTC 794
125 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
126 245 250 255
128 CTG AAC ACC TTC CAG GAA TTC TTT GGC CTG AAT AAT TGC AGT AGC TCT 842
129 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser

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130          260          265          270
132 AAC AGG TTG GAC CAA GCT ATG CAG GTG ACA GAG ACT CTT GGG ATG ACG      890
133 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
134          275          280          285
136 CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT GTC GGG GAG AAG TTC      938
137 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
138          290          295          300
140 AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC ATT GCC AAA CGC TTC      986
141 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
142 305          310          315          320
144 TGC AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT CCC GAG CGA GCA AGC      1034
145 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
146          325          330          335
147 TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA ATA TCT GTG GGC TTG      1082
148 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
149          340          345          350
151 TGACACGGAC TCAAGTGGGC TGGTGACCCA GTCAGAGTTG TGCACATGGC TTAGTTTTCA      1142
153 TACACAGCCT GGGCTGGGGG TGGGGTGGGA GAGGTCTTTT TTAAAAGGAA GTTACTGTTA      1202
155 TAGAGGTCT AAGATTCATC CAT                                  1225
158 (2) INFORMATION FOR SEQ ID NO: 2:
160     (i) SEQUENCE CHARACTERISTICS:
161         (A) LENGTH: 352 amino acids
162         (B) TYPE: amino acid
163         (D) TOPOLOGY: linear
165     (ii) MOLECULE TYPE: peptide
169     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
171 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
172 1          5          10          15
175 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
176          20          25          30
178 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
179          35          40          45
182 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
183          50          55          60
186 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
187 65          70          75          80
189 Leu Thr Val Pro Phe Trp Ala His Tyr Leu Ala Ala Gln Trp Asp Phe
190          85          90          95
193 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
194          100          105          110
197 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
198          115          120          125
201 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
202          130          135          140
205 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
206 145          150          155          160
209 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
210          165          170          175
213 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn

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214		180		185		190	
217	Phe Gln Thr	Leu Lys Ile Val	Ile Leu Gly Leu Val	Leu Pro Leu Leu			
218		195		200		205	
221	Val Met Val	Ile Cys Tyr Ser	Gly Ile Leu Lys Thr	Leu Leu Arg Cys			
222		210		215		220	
225	Arg Asn Glu	Lys Lys Arg His	Arg Ala Val Arg	Leu Ile Phe Thr Ile			
226	225		230		235		240
229	Met Ile Val	Tyr Phe Leu Phe	Trp Ala Pro Tyr	Asn Ile Val Leu Leu			
230		245		250		255	
233	Leu Asn Thr	Phe Gln Glu Phe	Phe Gly Leu Asn	Asn Cys Ser Ser Ser			
234		260		265		270	
237	Asn Arg Leu	Asp Gln Ala Met	Gln Val Thr Glu	Thr Leu Gly Met Thr			
238		275		280		285	
241	His Cys Cys	Ile Asn Pro Ile	Ile Tyr Ala Phe	Val Gly Glu Lys Phe			
242		290		295		300	
245	Arg Asn Tyr	Leu Leu Val Phe	Phe Gln Lys His	Ile Ala Lys Arg Phe			
246	305		310		315		320
249	Cys Lys Cys	Cys Ser Ile Phe	Gln Gln Glu Ala	Pro Glu Arg Ala Ser			
250		325		330		335	
252	Ser Val Tyr	Thr Arg Ser Thr	Gly Glu Gln Glu	Ile Ser Val Gly Leu			
253		340		345		350	352
257	(2) INFORMATION FOR SEQ ID NO: 3:						
259	(i) SEQUENCE CHARACTERISTICS:						
260	(A) LENGTH: 1225 base pairs						
261	(B) TYPE: nucleic acid						
262	(C) STRANDEDNESS: single						
263	(D) TOPOLOGY: linear						
265	(ii) MOLECULE TYPE: cDNA						
268	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:						
270	AAGAAACTCT CCCCGGGTGG AACAAG						
272	ATG GAT TAT	CAA GTG TCA	AGT CCA ATC	TAT GAC ATC	AAT TAT TAT	ACA	26 74
273	Met Asp Tyr	Gln Val Ser	Ser Pro Ile	Tyr Asp Ile	Asn Tyr Tyr	Thr	
274	1	5		10		15	
276	TCG GAG CCC	TGC CAA AAA	ATC AAT GTG	AAG CAA ATC	GCA GCC CGC	CTC	122
277	Ser Glu Pro	Cys Gln Lys	Ile Asn Val	Lys Gln Ile	Ala Ala Arg	Leu	
278		20		25		30	
279	CTG CCT CCG	CTC TAC TCA	CTG GTG TTC	ATC TTT GGT	TTT GTG GGC	AAC	170
280	Leu Pro Pro	Leu Tyr Ser	Leu Val Phe	Ile Phe Gly	Phe Val Gly	Asn	
281		35		40		45	
283	ATG CTG GTC	ATC CTC ATC	CTG ATA AAC	TGC AAA AGG	CTG AAG AGC	ATG	218
284	Met Leu Val	Ile Leu Ile	Leu Ile Asn	Cys Lys Arg	Leu Lys Ser	Met	
285	50		55		60		
287	ACT GAC ATC	TAC CTG CTC	AAC CTG GCC	ATC TCT GAC	CTG TTT TTC	CTT	266
288	Thr Asp Ile	Tyr Leu Leu	Asn Leu Ala	Ile Ser Asp	Leu Phe Phe	Leu	
289	65		70		75	80	
291	CTT ACT GTC	CCC TTC TGG	GCT CAC TAT	GCT GCC GCC	CAG TGG GAC	TTT	314
292	Leu Thr Val	Pro Phe Trp	Ala His Tyr	Ala Ala Ala	Gln Trp Asp	Phe	
293		85		90		95	
295	GGA AAT ACA	ATG TGT CAA	CTC TTG ACA	GGG CTC TAT	TTT ATA GGC	TTC	362

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296	Gly	Asn	Thr	Met	Cys	Gln	Leu	Leu	Thr	Gly	Leu	Tyr	Phe	Ile	Gly	Phe	
297				100					105					110			
299	TTC	TCT	GGA	ATC	TTC	TTC	ATC	ATC	CTC	CTG	ACA	ATC	GAT	AGG	TAC	CTG	410
300	Phe	Ser	Gly	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr	Ile	Asp	Arg	Tyr	Leu	
301			115					120					125				
303	GCT	GTC	GTC	CAT	GCT	GTG	TTT	GCT	TTA	AAA	GCC	AGG	ACG	GTC	ACC	TTT	458
304	Ala	Val	Val	His	Ala	Val	Phe	Ala	Leu	Lys	Ala	Arg	Thr	Val	Thr	Phe	
305		130						135					140				
307	GGG	GTG	GTG	ACA	AGT	GTG	ATC	ACT	TGG	GTG	GTG	GCT	GTG	TTT	GCG	TCT	506
308	Gly	Val	Val	Thr	Ser	Val	Ile	Thr	Trp	Val	Val	Ala	Val	Phe	Ala	Ser	
309	145					150					155				160		
311	CTC	CCA	GGA	ATC	ATC	TTT	ACC	AGA	TCT	CAA	AAA	GAA	GGT	CTT	CAT	TAC	554
312	Leu	Pro	Gly	Ile	Ile	Phe	Thr	Arg	Ser	Gln	Lys	Glu	Gly	Leu	His	Tyr	
313				165						170					175		
315	ACC	TGC	AGC	TCT	CAT	TTT	CCA	TAC	AGT	CAG	TAT	CAA	TTC	TGG	AAG	AAT	602
316	Thr	Cys	Ser	Ser	His	Phe	Pro	Tyr	Ser	Gln	Tyr	Gln	Phe	Trp	Lys	Asn	
317				180					185					190			
319	TTC	CAG	ACA	TTA	AAG	ATA	GTC	ATC	TTG	GGG	CTG	GTC	CTG	CCG	CTG	CTT	650
320	Phe	Gln	Thr	Leu	Lys	Ile	Val	Ile	Leu	Gly	Leu	Val	Leu	Pro	Leu	Leu	
321			195					200					205				
323	GTC	ATG	GTC	ATC	TGC	TAC	TCG	GGA	ATC	CTA	AAA	ACT	CTG	CTT	CGG	TGT	698
324	Val	Met	Val	Ile	Cys	Tyr	Ser	Gly	Ile	Leu	Lys	Thr	Leu	Leu	Arg	Cys	
325		210					215					220					
327	CGA	AAT	GAG	AAG	AAG	AGG	CAC	AGG	GCT	GTG	AGG	CTT	ATC	TTC	ACC	ATC	746
328	Arg	Asn	Glu	Lys	Lys	Arg	His	Arg	Ala	Val	Arg	Leu	Ile	Phe	Thr	Ile	
329	225				230					235					240		
331	ATG	ATT	GTT	TAT	TTT	CTC	TTC	TGG	GCT	CCC	TAC	AAC	ATT	GTC	CTT	CTC	794
332	Met	Ile	Val	Tyr	Phe	Leu	Phe	Trp	Ala	Pro	Tyr	Asn	Ile	Val	Leu	Leu	
333				245					250					255			
335	CTG	AAC	ACC	TTC	CAG	GAA	TTC	TTT	GGC	CTG	AAT	AAT	TGC	AGT	AGC	TCT	842
336	Leu	Asn	Thr	Phe	Gln	Glu	Phe	Phe	Gly	Leu	Asn	Asn	Cys	Ser	Ser	Ser	
337			260					265					270				
339	AAC	AGG	TTG	GAC	CAA	GCT	ATG	CAG	GTG	ACA	GAG	ACT	CTT	GGG	ATG	ACG	890
340	Asn	Arg	Leu	Asp	Gln	Ala	Met	Gln	Val	Thr	Glu	Thr	Leu	Gly	Met	Thr	
341			275					280					285				
343	CAC	TGC	TGC	ATC	AAC	CCC	ATC	ATC	TAT	GCC	TTT	GTC	GGG	GAG	AAG	TTC	938
344	His	Cys	Cys	Ile	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	Val	Gly	Glu	Lys	Phe	
345		290					295					300					
347	AGA	AAC	TAC	CTC	TTA	GTC	TTC	TTC	CAA	AAG	CAC	ATT	GCC	AAA	CGC	TTC	986
348	Arg	Asn	Tyr	Leu	Leu	Val	Phe	Phe	Gln	Lys	His	Ile	Ala	Lys	Arg	Phe	
349	305				310					315					320		
351	TGC	AAA	TGC	TGT	TCT	ATT	TTC	CAG	CAA	GAG	GCT	CCC	GAG	CGA	GCA	AGC	1034
352	Cys	Lys	Cys	Cys	Ser	Ile	Phe	Gln	Gln	Glu	Ala	Pro	Glu	Arg	Ala	Ser	
353				325					330				335				
354	TCA	GTT	TAC	ACC	CGA	TCC	ACT	GGG	GAG	CAG	GAA	ATA	TCT	GTG	GGC	TTG	1082
355	Ser	Val	Tyr	Thr	Arg	Ser	Thr	Gly	Glu	Gln	Glu	Ile	Ser	Val	Gly	Leu	
356			340					345					350				
358	TGACACGGAC	TCAAGTGGGC	TGGTGACCCA	GTCAGAGTTG	TGCACATGGC	TTAGTTTTCA											1142
360	TACACAGCCT	GGGCTGGGGG	TGGGGTGGGA	GAGGTCTTTT	TAAAAAGGAA	GTTACTGTTA											1202

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos.1

VERIFICATION SUMMARY

DATE: 08/27/2004

PATENT APPLICATION: US/10/700,313

TIME: 14:23:01

Input Set : N:\CrF3\RULE60\10700313.raw

Output Set: N:\CRF4\08272004\J700313.raw

L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:34 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:37 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:39 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:44 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]
L:474 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:479 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0